2. Induction of an immune mechanism maintains an immune inflamatory reaction in the liver sharing in the pathogenisis of cirrhosis.
3. Patients showing unexpected deterioration in liver functions or decompensation of hepatic cirrhosis must do blood cultures and receive antibiotics.

PP-082 Diagnosis of *Helicobacter pylori* infection by ELISA stool antigen and comparison with other diagnostic methods

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During the last decade, the role of *Helicobacter pylori* (*H. pylori*) infections in pathogenesis of gastric ulcers in adults and children has been well defined. Stool samples were collected from 116 adults who were undergoing endoscopic examinations and stomach biopsies and for whom histology and rapid urease tests were performed. In our research, we used a monoclonal antibody as the capturing antibody and a polyclonal antibody of rabbit origin conjugated with a peroxidase enzyme as the tracer. The results obtained in this study were compared with those from the histology and rapid urease tests, which are considered to be the "gold standard"; in addition, the correlation between our results and those from two conventional tests, i.e., rapid immuno-chromatography by the Certest Company and ELISA by the Astra Company, was investigated.

In the histology and rapid urease tests, 21 of the 116 patients (18.1%) had positive results. *H. pylori* antigens were detected by the designed method in 19 of 21 cases (a sensitivity of 91%). Also, all of the 95 cases with negative results in the histology and rapid urease tests were negative for the stool antigen test (a specificity of 100%). For comparison, the sensitivity and specificity of the rapid immuno-chromatography test by the Certest Company were 95% and 99%, respectively. The total correlations between the results of the designed ELISA test with the results of the rapid test and the ELISA test of the Astra Company were 96% and 80%, respectively.

This non-invasive and economical method for the detection of *H. pylori* antigens in stool can be considered as an alternative test that provides comparable reliability and validity to the histology and rapid urease tests for the detection of *H. pylori* infections.

PP-083 Determination of peroxisome proliferator-activated receptor-gamma polymorphism with *Helicobacter pylori* infection in Iran

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Objectives: Peroxisome proliferator-activated receptor (PPAR), a member of the nuclear hormone receptor super family initially shown to be a key regulator of fat cell differentiation, can inhibit cell growth and induce apoptosis in colon cell lines. A common structural polymorphism in the *PPAR* gene, CCA/GCA, producing a Pro/Ala substitution at codon 12 (Pro12Ala), has been detected. The Pro12Ala polymorphism could plausibly play a role in the etiology of colorectal adenomas, a precursor lesion of colorectal cancer. Helicobacter pylori (Hp) infections can cause gastritis, duodenal ulcer, gastric cancer or peptic ulcer. The aim of this study was determination polymorphism PPAR-γ gene among Hp positive patients in Iran.

Methods: In this study blood of 200 Helicobacter pylori infected patients with gastric cancer and 200 matched controls that confirmed by ELISA test were collected. Peroxisome proliferator-activated receptor (PPAR) Pro12Ala polymorphism was analyzed by polymerase chain reaction-restriction fragment length polymorphism.

Results: By PCR-RFLP on 200 DNA isolated samples, 3 polymorphism templates were detected on their PCR products (Table 1). The frequency of G allele was significantly higher among Helicobacter pylori infected patients with gastric cancer (41.5%) than in control (9.6%, OR 3.2, 95% CI 1.7–6.4).

Conclusion: These results suggest that there is a significant association between peroxisome proliferator-activated receptor-gamma polymorphism and Helicobacter pylori infected patients with gastric cancer in Iran.

Table 1. Frequency of peroxisome proliferator-activated receptor-gamma polymorphism in gastric cancer patients and controls

PPAR-γ genotype	Cases (200)	Controls (200)	OR (95%CI)	P-value
CC	117 (58.5%)	179 (89.5%)	2.3 (1.2–5.4)	0.09
G carriers	83 (41.5)	21 (10.5%)	8.1 (2.5–61.3)	0.0006

PP-084 Characterization of class 1 integron resistance gene cassettes and *Salmonella* genomic island 1 among *Salmonella* strains from healthy humans in Northern China

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Objectives: The aim of this study was to analyse the distribution and effect on the antibiotic resistance mechanisms of class 1 integrons and *Salmonella* genomic island 1 (SGI1) in *Salmonella* strains obtained from healthy humans in China.

Methods: Fifty-eight *Salmonella* strains of 25 serovars isolated from healthy humans in Shijiazhuang, northern China, in 2005 and 2007 were tested for susceptibility to 15 common antibiotics and the presence of class 1 integrons.

Results: Fifty-one strains (87.9%) were resistant to at least one antibiotic; the most common resistance phenotype was to streptomycin (82.8%). Five strains were positive for the class 1 integrase gene (*intI1*), three in 2005 and two in 2007. Three different cassette arrays were detected: *aadA2*, bla_{PSE-1}, and *dfrA12-orfF-aadA2*. Plasmid conjugation indicated that all the detected integrons were on plasmids and could transfer to other strains. Sau-PCR showed that there was no direct correlation between the integron-positive and integron-negative strains. SGI1 was detected in a *S.* Typhimurium strain, with the *aadA2*, *floR*, *tetG*, and bla_{PSE-1} genes in its multidrug resistance region, and it was located between *thdF* and a retronphage (*int2*).

Conclusions: To our knowledge, this is the first report on SGI1 in strains from healthy humans. The presence of class 1 integrons and SGI1 in *Salmonella* strains from healthy humans suggests that widespread surveillance of antibiotic resistance should be conducted at the gene level.

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